AMENDMENTS TO THE CLAIMS:

Please amend claims 175, 188, 195, 196 and 207 as shown in the following list of the claims:

1.-121. (Canceled).

122. (Previously Presented) A method of assessing the effectiveness of protease antiretroviral therapy of a patient infected with HIV, said method comprising detecting in a biological sample from said HIV-infected patient a nucleic acid encoding an HIV protease that comprises a mutation at codon 82 and a secondary mutation at a codon selected from the group consisting of codons 55, 43, 53, 13, 23, 33, 74, 32, 39, 60, and 35, wherein the presence of said protease-encoding nucleic acid in said biological sample indicates a difference in said HIV protease's susceptibility to amprenavir relative to a reference HIV protease, thereby assessing the effectiveness of protease antiretroviral therapy.

123. (Previously Presented) The method of Claim 122, wherein said mutation at codon 82 is a substitution of alanine (A), phenylalanine (F), serine (S), or threonine (T) for valine (V).

124. (Previously Presented) The method of Claim 122, wherein said nucleic acid has a mutation at codon 82 and a secondary mutation at a codon selected from the group consisting of codons 55, 43, 53, 13, 23, 74, 60, 33, 35, and 32, and wherein the presence of said protease-encoding nucleic acid in said biological sample indicates a difference in said HIV protease's susceptibility to amprenavir relative to a reference HIV protease, thereby assessing the effectiveness of protease antiretroviral therapy.

125. (Previously Presented) The method of claim 124, wherein said difference in said HIV's susceptibility to amprenavir relative to a reference HIV is greater than 10 fold.

126. (Previously Presented) A method of assessing the effectiveness of protease antiretroviral therapy of a patient infected with HIV, said method comprising detecting in a biological sample from said patient a nucleic acid encoding HIV protease having a mutation at codon 82 and a secondary mutation at a codon selected from the group consisting of codons 33, 23, 32, 53, 37, 71, 61, 11, and 46, wherein the

presence of said protease-encoding nucleic acid in said biological sample indicates a difference in said HIV protease's susceptibility to amprenavir relative to a reference HIV protease, thereby assessing the effectiveness of protease antiretroviral therapy.

127. (Previously Presented) A method of assessing the effectiveness of protease antiretroviral therapy of a patient infected with HIV, said method comprising detecting in a biological sample from said HIV-infected patient a nucleic acid encoding an HIV protease that comprises a mutation at codon 82 and a secondary mutation at a codon selected from the group consisting of codons 55, 53, 23, 33, and 39, wherein the presence of said protease-encoding nucleic acid in said biological sample indicates a difference in said HIV protease's susceptibility to a protease inhibitor relative to a reference HIV protease, thereby assessing the effectiveness of protease antiretroviral therapy.

128. (Previously Presented) The method of Claim 127, wherein said mutation at codon 82 is a substitution of alanine (A), phenylalanine (F), serine (S), or threonine (T) for valine (V), and wherein the presence of said protease-encoding nucleic acid in said biological sample indicates a difference in said HIV protease's susceptibility to a protease inhibitor relative to a reference HIV protease, thereby assessing the effectiveness of protease antiretroviral therapy.

129. (Previously Presented) The method of Claim 127, wherein said protease inhibitor is selected from the group consisting of indinavir, amprenavir, and saquinavir and wherein the presence of said protease-encoding nucleic acid in said biological sample indicates a difference in said HIV protease's susceptibility to said protease inhibitor, which is selected from relative to a reference HIV protease, thereby assessing the effectiveness of protease antiretroviral therapy.

130. (Previously Presented) The method of Claim 129, wherein said nucleic acid has a mutation at codon 82 and a secondary mutation at a codon selected from the group consisting of codons 23, 53, 33, and 39, and wherein said protease inhibitor is saquinavir.

131. (Previously Presented) The method of Claim 129, wherein said nucleic acid has a mutation at codon 82 and a secondary mutation at a codon selected from the group consisting of codons 23, 53, and 33, wherein said difference in said HIV protease's

susceptibility to a protease inhibitor relative to a reference HIV protease is a decrease in susceptibility to saquinavir.

132. - 133. (Canceled).

134. (Previously Presented) The method of Claim 129, wherein said nucleic acid has a mutation at codon 82 and a secondary mutation at a codon selected from the group consisting of codons 55, 53, 23, and 33.

135. (Previously Presented) The method of claim 127, wherein said difference in said HIV protease's susceptibility to said protease inhibitor relative to a reference HIV is greater than 10 fold.

136. (Previously Presented) The method of claim 128, wherein said nucleic acid has a mutation at codon 82 and a secondary mutation at a codon selected from the group consisting of codons 23, 53, 33, and 35, and wherein said difference in said HIV protease's susceptibility to a protease inhibitor relative to a reference HIV protease is a decrease in susceptibility to saquinavir.

137. (Previously Presented) The method of claim 128, wherein said nucleic acid has a mutation at codon 82 and a secondary mutation at a codon selected from the group consisting of codons 55 and 53, and wherein said difference in said HIV protease's susceptibility to a protease inhibitor relative to a reference HIV protease is a decrease in susceptibility to indinavir.

138. (Previously Presented) A method of assessing the effectiveness of protease antiretroviral therapy of a patient infected with HIV, said method comprising detecting in a biological sample from said patient a nucleic acid encoding HIV protease having a mutation at codon 82 and a secondary mutation at a codon selected from the group consisting of codons 33, 23, 53, and 11, wherein the presence of said protease-encoding nucleic acid in said biological sample indicates a decrease in said HIV protease's susceptibility to a protease inhibitor relative to a reference HIV protease, thereby indicating a decrease in the effectiveness of protease antiretroviral therapy.

139. (Previously Presented) A method of assessing the effectiveness of protease antiretroviral therapy of a patient infected with HIV, said method comprising

detecting in a biological sample from said HIV-infected patient a nucleic acid encoding an HIV protease that comprises a mutation at codon 82 and a secondary mutation at a codon selected from the group consisting of codons 32 and 46; the group consisting of codons 13 and 61; or the group consisting of codons 32 and 39, wherein the presence of said protease-encoding nucleic acid in said biological sample indicates an increase in said HIV protease's susceptibility to a protease inhibitor relative to a reference HIV protease, thereby indicating an increase in the effectiveness of protease antiretroviral therapy.

140. (Previously Presented) The method of Claim 139, wherein said mutation at codon 82 is a substitution of alanine (A), phenylalanine (F), serine (S), or threonine (T) for valine (V).

141. (Previously Presented) The method of Claim 139, wherein said protease inhibitor is selected from the group consisting of indinavir, amprenavir, and saquinavir, and wherein the presence of said protease-encoding nucleic acid in said biological sample indicates a difference in said HIV protease's susceptibility to said protease inhibitor, which is selected from relative to a reference HIV protease, thereby assessing the effectiveness of protease antiretroviral therapy.

142. (Canceled).

143. (Previously Presented) The method of Claim 141, wherein said nucleic acid has a mutation at codon 82 and a secondary mutation at codon 32 or codon 39, and wherein said protease inhibitor is saquinavir.

144. (Canceled).

145. (Previously Presented) The method of Claim 141, wherein said nucleic acid has a mutation at codon 82 and a secondary mutation at codon 13, and wherein said protease inhibitor is indinavir.

146. (Canceled).

147. (Previously Presented) The method of claim 139, wherein said increase in said HIV protease's susceptibility to said protease inhibitor relative to a reference HIV protease is greater than 10 fold.

148. (Previously Presented) The method of claim 139, wherein the nucleic acid has a mutation at codon 82 and a secondary mutation at codon 32 or codon 46, and wherein said protease inhibitor is saquinavir.

149.-150. (Canceled).

151. (Previously Presented) The method of Claim 122, wherein said nucleic acid has a mutation at codon 82 and a secondary mutation at a codon 53.

152. (Previously Presented) The method of Claim 122, wherein said nucleic acid has a mutation at codon 82 and a secondary mutation at a codon 23.

153. (Previously Presented) The method of Claim 122, wherein said nucleic acid has a mutation at codon 82 and a secondary mutation at a codon 33.

154. (Previously Presented) The method of Claim 122, wherein said nucleic acid has a mutation at codon 82 and a secondary mutation at a codon 32.

155. (Previously Presented) The method of Claim 122, wherein said nucleic acid has a mutation at codon 82 and a secondary mutation at a codon 60.

156. (Previously Presented) The method of Claim 127, wherein said nucleic acid has a mutation at codon 82 and a secondary mutation at a codon 55.

157. (Previously Presented) The method of Claim 127, wherein said nucleic acid has a mutation at codon 82 and a secondary mutation at a codon 53.

158. (Previously Presented) The method of Claim 127, wherein said nucleic acid has a mutation at codon 82 and a secondary mutation at a codon 23.

159. (Previously Presented) The method of Claim 127, wherein said nucleic acid has a mutation at codon 82 and a secondary mutation at a codon 33.

160. (Previously Presented) The method of Claim 127, wherein said nucleic acid has a mutation at codon 82 and a secondary mutation at a codon 39.

161. (Previously Presented) The method of Claim 139, wherein said nucleic acid has a mutation at codon 82 and a secondary mutation at a codon 32.

162. (Previously Presented) The method of Claim 139, wherein said nucleic acid has a mutation at codon 82 and a secondary mutation at a codon 46.

163. (Previously Presented) The method of Claim 139, wherein said nucleic acid has a mutation at codon 82 and a secondary mutation at a codon 13.

164. (Previously Presented) The method of Claim 139, wherein said nucleic acid has a mutation at codon 82 and a secondary mutation at a codon 61.

165. (Previously Presented) The method of Claim 139, wherein said nucleic acid has a mutation at codon 82 and a secondary mutation at a codon 39.

166. (Previously Presented) A method of assessing the effectiveness of protease antiretroviral therapy of a patient infected with HIV, said method comprising detecting in a biological sample from said HIV-infected patient a nucleic acid encoding an HIV protease that comprises a mutation at codon 90 and a secondary mutation at a codon selected from the group consisting of codons 53, 95, 13, 74, 55, 85, 62, 66, 33, 64, 23, and 58, wherein the presence of said protease-encoding nucleic acid in said biological sample indicates a difference in said HIV protease's susceptibility to amprenavir relative to a reference HIV protease, thereby assessing the effectiveness of protease antiretroviral therapy.

167. (Previously Presented) The method of Claim 166, wherein said nucleic acid has a mutation at codon 90 and a secondary mutation at a codon 53.

168. (Previously Presented) The method of Claim 166, wherein said nucleic acid has a mutation at codon 90 and a secondary mutation at a codon 95.

169. (Previously Presented) The method of Claim 166, wherein said nucleic acid has a mutation at codon 90 and a secondary mutation at a codon 13.

170. (Previously Presented) The method of Claim 166, wherein said nucleic acid has a mutation at codon 90 and a secondary mutation at a codon 74.

171. (Previously Presented) The method of Claim 166, wherein said nucleic acid has a mutation at codon 90 and a secondary mutation at a codon 55.

172. (Previously Presented) The method of Claim 166, wherein said nucleic acid has a mutation at codon 90 and a secondary mutation at a codon 66.

173. (Previously Presented) The method of Claim 166, wherein said nucleic acid has a mutation at codon 90 and a secondary mutation at a codon 33.

174. (Previously Presented) The method of Claim 166, wherein said mutation at codon 90 is a substitution of methionine (M) for leucine (L).

175. (Currently Amended) The method of Claim 166, wherein said nucleic acid has a mutation at codon 90 and a secondary mutation at a codon selected from the group consisting of codons 95, 55, 85, 62, 74, 53, 23, 58, ~~64 and 77~~ and 64, and wherein the presence of said protease-encoding nucleic acid in said biological sample indicates a difference in said HIV protease's susceptibility to amprenavir relative to a reference HIV protease, thereby assessing the effectiveness of protease antiretroviral therapy.

176. (Previously Presented) The method of claim 175, wherein said difference in said HIV's susceptibility to amprenavir relative to a reference HIV is greater than 10 fold.

177. (Previously Presented) A method of assessing the effectiveness of protease antiretroviral therapy of a patient infected with HIV, said method comprising detecting in a biological sample from said patient a nucleic acid encoding HIV protease having a mutation at codon 90-and a secondary mutation at a codon selected from the group consisting of codons 89, 53, 33, 92, 95, 58, 62, 74, 15, 47, 66, 32, 55, 53, 13, and 69, wherein the presence of said protease-encoding nucleic acid in said biological sample in comparison indicates a difference in said HIV protease's susceptibility to amprenavir relative to a reference HIV protease, thereby assessing the effectiveness of protease antiretroviral therapy.

178. (Previously Presented) A method of assessing the effectiveness of protease antiretroviral therapy of a patient infected with HIV, said method comprising detecting in a biological sample from said HIV-infected patient a nucleic acid encoding an HIV protease that comprises a mutation at codon 90 and a secondary mutation at a codon selected from the group consisting of codons 53, 95, 55, 85, 66, 33, 23, and 58, wherein the presence of said protease-encoding nucleic acid in said biological sample indicates a difference in said HIV protease's susceptibility to a

protease inhibitor relative to a reference HIV protease, thereby assessing the effectiveness of protease antiretroviral therapy.

179. (Previously Presented) The method of Claim 178, wherein said nucleic acid has a mutation at codon 90 and a secondary mutation at a codon 53.

180. (Previously Presented) The method of Claim 178, wherein said nucleic acid has a mutation at codon 90 and a secondary mutation at a codon 95.

181. (Previously Presented) The method of Claim 178, wherein said nucleic acid has a mutation at codon 90 and a secondary mutation at a codon 55.

182. (Previously Presented) The method of Claim 178, wherein said nucleic acid has a mutation at codon 90 and a secondary mutation at a codon 85.

183. (Previously Presented) The method of Claim 178, wherein said nucleic acid has a mutation at codon 90 and a secondary mutation at a codon 66.

184. (Previously Presented) The method of Claim 178, wherein said nucleic acid has a mutation at codon 90 and a secondary mutation at a codon 33.

185. (Previously Presented) The method of Claim 178, wherein said nucleic acid has a mutation at codon 90 and a secondary mutation at a codon 23.

186. (Previously Presented) The method of Claim 178, wherein said nucleic acid has a mutation at codon 90 and a secondary mutation at a codon 58.

187. (Previously Presented) The method of Claim 178, wherein said mutation at codon 90 is a substitution of methionine (M) for leucine (L) , and wherein the presence of said protease-encoding nucleic acid in said biological sample indicates a difference in said HIV protease's susceptibility to a protease inhibitor relative to a reference HIV protease, thereby assessing the effectiveness of protease antiretroviral therapy.

188. (Currently Amended) The method of Claim 178, wherein said protease inhibitor is selected from the group consisting of indinavir, amprenavir, and saquinavir and wherein the presence of said protease-encoding nucleic acid in said biological sample indicates a difference in said HIV protease's susceptibility to said protease inhibitor

[[,]] ~~which is selected from~~ relative to a reference HIV protease, thereby assessing the effectiveness of protease antiretroviral therapy.

189. (Previously Presented) The method of Claim 188, wherein said nucleic acid has a mutation at codon 90 and a secondary mutation at a codon selected from the group consisting of codons 53, 66, and 33, and wherein said protease inhibitor is saquinavir.

190. (Previously Presented) The method of Claim 188, wherein said nucleic acid has a mutation at codon 90 and a secondary mutation at a codon selected from the group consisting of codons 53, 66, and 33, wherein said difference in said HIV protease's susceptibility to a protease inhibitor relative to a reference HIV protease is a decrease in susceptibility to saquinavir.

191. (Previously Presented) The method of Claim 188, wherein said nucleic acid has a mutation at codon 90 and a secondary mutation at a codon selected from the group consisting of codons 53 and 95, and wherein said protease inhibitor is indinavir.

192. (Previously Presented) The method of Claim 188, wherein said nucleic acid has a mutation at codon 90 and a secondary mutation at a codon selected from the group consisting of codons 53 and 95, and wherein said difference in said HIV protease's susceptibility to a protease inhibitor relative to a reference HIV protease is a decrease in susceptibility to indinavir.

193. (Previously Presented) The method of Claim 188, wherein said nucleic acid has a mutation at codon 90 and a secondary mutation at a codon selected from the group consisting of codons 95, 55, 85, 53, 23, 58, and 77.

194. (Previously Presented) The method of claim 178, wherein said difference in said HIV protease's susceptibility to said protease inhibitor relative to a reference HIV is greater than 10 fold.

195. (Currently Amended) The method of claim ~~179~~ 178, wherein said nucleic acid has a mutation at codon 90 and a secondary mutation at a codon selected from the group consisting of codons 53, 23, and 58, and wherein said difference in said HIV protease's susceptibility to a protease inhibitor relative to a reference HIV protease is a decrease in susceptibility to saquinavir.

196. (Currently Amended) The method of claim ~~179~~ 178, wherein said nucleic acid has a mutation at codon 90 and a secondary mutation at a codon selected from the group consisting of codons 95, 55, and 85, and wherein said difference in said HIV protease's susceptibility to a protease inhibitor relative to a reference HIV protease is a decrease in susceptibility to indinavir.

197. (Previously Presented) A method of assessing the effectiveness of protease antiretroviral therapy of a patient infected with HIV, said method comprising detecting in a biological sample from said patient a nucleic acid encoding HIV protease having a mutation at codon 90 and a secondary mutation at a codon selected from the group consisting of codons 89, 53, 33, 92, 95, 58, 66, and 55, wherein the presence of said protease-encoding nucleic acid in said biological sample indicates a decrease in said HIV protease's susceptibility to a protease inhibitor relative to a reference HIV protease, thereby indicating a decrease in the effectiveness of protease antiretroviral therapy.

198. (Previously Presented) A method of assessing the effectiveness of protease antiretroviral therapy of a patient infected with HIV, said method comprising detecting in a biological sample from said HIV-infected patient a nucleic acid encoding an HIV protease that comprises a mutation at codon 90 and a secondary mutation at a codon selected from the group consisting of codons 64, 77, and 93; the group consisting of codons 13 and 74; or the group consisting of codons 74, 15, and 69, wherein the presence of said protease-encoding nucleic acid in said biological sample indicates an increase in said HIV protease's susceptibility to a protease inhibitor relative to a reference HIV protease, thereby indicating an increase in the effectiveness of protease antiretroviral therapy.

199. (Previously Presented) The method of Claim 198, wherein said nucleic acid has a mutation at codon 90 and a secondary mutation at a codon 64.

200. (Previously Presented) The method of Claim 198, wherein said nucleic acid has a mutation at codon 90 and a secondary mutation at a codon 77.

201. (Previously Presented) The method of Claim 198, wherein said nucleic acid has a mutation at codon 90 and a secondary mutation at a codon 93.

202. (Previously Presented) The method of Claim 198, wherein said nucleic acid has a mutation at codon 90 and a secondary mutation at a codon 13.

203. (Previously Presented) The method of Claim 198, wherein said nucleic acid has a mutation at codon 90 and a secondary mutation at a codon 74.

204. (Previously Presented) The method of Claim 198, wherein said nucleic acid has a mutation at codon 90 and a secondary mutation at a codon 15.

205. (Previously Presented) The method of Claim 198, wherein said nucleic acid has a mutation at codon 90 and a secondary mutation at a codon 69.

206. (Previously Presented) The method of Claim 198, wherein said mutation at codon 90 is a substitution of methionine (M) for leucine (L).

207. (Currently Amended) The method of Claim 198, wherein said protease inhibitor is selected from the group consisting of indinavir, amprenavir, and saquinavir and wherein the presence of said protease-encoding nucleic acid in said biological sample indicates a difference in said HIV protease's susceptibility to said protease inhibitor [[,]] ~~which is selected from~~ relative to a reference HIV protease, thereby assessing the effectiveness of protease antiretroviral therapy.

208. (Previously Presented) The method of Claim 207, wherein said nucleic acid has a mutation at codon 90 and a secondary mutation at codon 64 or codon 93, and wherein said protease inhibitor is saquinavir.

209. (Previously Presented) The method of Claim 207, wherein said nucleic acid has a mutation at codon 90 and a secondary mutation at codon 13 or codon 74, and wherein said protease inhibitor is indinavir.

210. (Previously Presented) The method of claim 198, wherein said increase in said HIV protease's susceptibility to said protease inhibitor relative to a reference HIV protease is greater than 10 fold.

211. (Previously Presented) The method of claim 198, wherein the nucleic acid has a mutation at codon 90 and a secondary mutation at codon 64, codon 77, or codon 93, and wherein said protease inhibitor is saquinavir.